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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=1; day=14; hr=11; min=45; sec=0; ms=652;]

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Application No: 10500240 Version No: 4.0

Input Set:

Output Set:

Started: 2008-12-31 11:18:48.658
Finished: 2008-12-31 11:18:55.043
Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 385 ms
Total Warnings: 23
Total Errors: 30
No. of SeqIDs Defined: 106
Actual SeqID Count: 106

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

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Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
E 257	Invalid sequence data feature in <221> in SEQ ID (24)
E 257	Invalid sequence data feature in <221> in SEQ ID (24)
E 257	Invalid sequence data feature in <221> in SEQ ID (26)
E 257	Invalid sequence data feature in <221> in SEQ ID (36)
E 257	Invalid sequence data feature in <221> in SEQ ID (38)
E 257	Invalid sequence data feature in <221> in SEQ ID (38)
E 257	Invalid sequence data feature in <221> in SEQ ID (40)
E 257	Invalid sequence data feature in <221> in SEQ ID (40)
E 257	Invalid sequence data feature in <221> in SEQ ID (42)
E 257	Invalid sequence data feature in <221> in SEQ ID (42)
E 257	Invalid sequence data feature in <221> in SEQ ID (54)
E 257	Invalid sequence data feature in <221> in SEQ ID (56)
E 257	Invalid sequence data feature in <221> in SEQ ID (58)
E 257	Invalid sequence data feature in <221> in SEQ ID (60)
E 257	Invalid sequence data feature in <221> in SEQ ID (62)
E 257	Invalid sequence data feature in <221> in SEQ ID (68)
E 257	Invalid sequence data feature in <221> in SEQ ID (70)
E 257	Invalid sequence data feature in <221> in SEQ ID (72)
E 257	Invalid sequence data feature in <221> in SEQ ID (78)
E 257	Invalid sequence data feature in <221> in SEQ ID (78) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> WILDT, Stefan
MIELE, Robert G.
NETT, Juergen H.
DAVIDSON, Robert C.

<120> METHODS TO ENGINEER MAMMALIAN-TYPE
CARBOHYDRATE STRUCTURES

<130> GF0022P

<140> 10500240
<141> 2005-03-23

<150> PCT/US02/41510
<151> 2002-12-24

<150> 60/344,169
<151> 2001-12-27

<160> 106

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<220>
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<220>
<223> Primer

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<220>
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<210> 8	
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<210> 9

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

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<400> 9

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<211> 24

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<213> Artificial Sequence

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<220>

<223> Primer

<400> 11

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<210> 12

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 12

gatttataga catgaaccat tggctcggtt tcgacactgg atgg 44

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<211> 20

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<220>

<223> Primer

<400> 13

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<210> 14
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<220>
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27

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<211> 36
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<223> Primer

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<213> Artificial Sequence

<220>
<223> Primer

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28

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<213> Artificial Sequence

<220>
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<400> 18
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28

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<223> Primer

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<220>
<223> Primer

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29

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<220>
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27

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<220>
<223> Primer

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28

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<213> *Saccharomyces cerevisiae*

<400> 23
His Asp Glu Leu
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<210> 24
<211> 458
<212> PRT
<213> *Saccharomyces cerevisiae*

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<222> (304) ... (318)
<223> Xaa is a variable amino acid
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<222> (416) ... (436)
<223> Xaa is a variable amino acid
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 20 25 30
 Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
 35 40 45
 Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys
 50 55 60
 Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
 65 70 75 80
 Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
 85 90 95
 Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
 100 105 110
 Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
 115 120 125
 Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
 130 135 140
 Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
 145 150 155 160
 Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
 165 170 175
 Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
 180 185 190
 Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
 195 200 205
 Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
 210 215 220
 Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
 225 230 235 240
 Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
 245 250 255
 Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
 260 265 270
 His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
 275 280 285
 Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe Xaa
 290 295 300
 Xaa Phe Val
 305 310 315 320
 Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His
 325 330 335
 Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile
 340 345 350
 Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg
 355 360 365

Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile
 370 375 380
 Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr
 385 390 395 400
 Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Xaa
 405 410 415
 Xaa
 420 425 430
 Xaa Xaa Xaa Xaa Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg
 435 440 445
 Thr Thr Ser Ser Met Glu Lys Lys Leu Asn
 450 455

<210> 25
 <211> 458
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 25
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 1 5 10 15
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 20 25 30
 Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
 35 40 45
 Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys
 50 55 60
 Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
 65 70 75 80
 Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
 85 90 95
 Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
 100 105 110
 Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
 115 120 125
 Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
 130 135 140
 Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
 145 150 155 160
 Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
 165 170 175
 Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
 180 185 190
 Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
 195 200 205
 Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
 210 215 220
 Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
 225 230 235 240
 Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
 245 250 255
 Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
 260 265 270
 His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
 275 280 285
 Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His

290	295	300
Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val		
305	310	315
Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His		320
325	330	335
Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile		
340	345	350
Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg		
355	360	365
Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile		
370	375	380
Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr		
385	390	395
Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala		400
405	410	415
Ser Thr Leu Leu Ala Leu Asn Thr Val Leu Leu Leu Leu Ala		
420	425	430
Leu Thr Gln Leu Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg		
435	440	445
Thr Thr Ser Ser Met Glu Lys Lys Leu Asn		
450	455	

<210> 26
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<212> PRT
<213> *Saccharomyces cerevisiae*

<220>
<221> MOD_RES
<222> (333) ... (347)
<223> Xaa is a variable amino acid

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20	25	30
Cys Lys Ile Ile Ile Lys Lys Val Ala Tyr Thr Glu Ile Asp Tyr Lys		
35	40	45
Ala Tyr Met Glu Gln Ile Glu Met Ile Gln Leu Asp Gly Met Leu Asp		
50	55	60
Tyr Ser Gln Val Ser Gly Gly Thr Gly Pro Leu Val Tyr Pro Ala Gly		
65	70	75
His Val Leu Ile Tyr Lys Met Met Tyr Trp Leu Thr Glu Gly Met Asp		
85	90	95
His Val Glu Arg Gly Gln Val Phe Phe Arg Tyr Leu Tyr Leu Leu Thr		
100	105	110
Leu Ala Leu Gln Met Ala Cys Tyr Tyr Leu Leu His Leu Pro Pro Trp		
115	120	125
Cys Val Val Leu Ala Cys Leu Ser Lys Arg Leu His Ser Ile Tyr Val		
130	135	140
Leu Arg Leu Phe Asn Asp Cys Phe Thr Thr Leu Phe Met Val Val Thr		
145	150	155
Val Leu Gly Ala Ile Val Ala Ser Arg Cys His Gln Arg Pro Lys Leu		
165	170	175
Lys Lys His Gln Thr Cys Lys Val Pro Pro Phe Val Phe Phe Met		

180	185	190
Cys Cys Ala Ser Tyr Arg Val His Ser Ile Phe Val Leu Arg	Leu Phe	
195	200	205
Asn Asp Pro Val Ala Met Val Leu Leu Phe Leu Ser Ile Asn	Leu Leu	
210	215	220
Leu Ala Gln Arg Trp Gly Trp Gly Ser Leu Ala Leu Val Ile	Ser Ala	
225	230	235
Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu	Leu Tyr Phe	
245	250	255
Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala	Asn Val Ile	
260	265	270
Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln	Val Ala Val	
275	280	285
Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu	His Cys Ala	
290	295	300
Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile Asn	Trp Gln	
305	310	315
Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe Xaa	Xaa Xaa Xaa Xaa	
325	330	335
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Val Thr Arg	Tyr	
340	345	350
Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His	Pro Leu Arg	
355	360	365
Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile	Pro Phe Val	
370	375	380
Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg	Ser Leu His	
385	390	395
Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile	Leu Ile Phe	
405	410	415
Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr	Val Leu His	
420	425	430
Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser		
435	440	

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<211> 373
<212> PRT
<213> Homo sapiens

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20	25	30
Ile His Arg Val Ala Tyr Thr Glu Ile Asp Trp Lys	Ala Tyr Met Ala	
35	40	45
Glu Val Glu Gly Val Gly Thr Tyr Asp Tyr Thr Gln	Leu Gln Gly Asp	
50	55	60
Thr Gly Pro Leu Val Tyr Pro Ala Gly Phe Val	Tyr Ile Phe Met Gly	
65	70	75
Leu Tyr Tyr Ala Thr Ser Arg Gly Thr Asp Ile Arg	Met Ala Gln Asn	
85	90	95
Ile Phe Ala Val Leu Tyr Leu Ala Thr Leu Leu Val	Phe Leu Ile	
100	105	110
Tyr His Gln Thr Cys Lys Val Pro Pro Phe Val Phe	Phe Met Cys	
115	120	125

Cys Ala Ser Tyr Arg Val His Ser Ile Phe Val Leu Arg Leu Phe Asn
130 135 140
Asp Pro Val Ala Met Val Leu Leu Phe Leu Ser Ile Asn Leu Leu Leu
145 150 155 160
Ala Gln Arg Trp Gly Trp Gly Cys Cys Phe Phe Ser Leu Ala Val Ser
165 170 175
Val Lys Met Asn Val Leu Leu Phe Ala Pro Gly Leu Leu Phe Leu Leu
180 185 190
Leu Thr Gln Phe Gly Phe Arg Gly Ala Leu Pro Lys Leu Gly Ile Cys
195 200 205
Ala Gly Leu Gln Val Val Leu Gly Leu Pro Phe Leu Leu Glu Asn Pro
210 215 220
Ser Gly Tyr Leu Ser Arg Ser Phe Asp Leu Gly Arg Gln Phe Leu Phe
225 230 235